

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2001, 15:18:17 ; Search time 2977.57 Seconds
(without alignments)
513.469 Million cell updates/sec

Title: US-09-593-316-3
Perfect score: 1617
Sequence: 1 ccggagggccggccgagctg.....attgagagatattattct 1617

Scoring table:
IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: qb_est1:*
2: qb_est2:*
3: qb_est3:*
4: qb_est4:*
5: qb_est5:*
6: qb_est6:*
7: qb_est7:*
8: qb_est8:*
9: qb_est9:*
10: qb_est10:*
11: qb_est11:*
12: qb_est12:*
13: qb_est13:*
14: qb_est14:*
15: qb_est15:*
16: qb_est16:*
17: qb_est17:*
18: qb_est18:*
19: qb_est19:*
20: qb_est20:*
21: qb_est21:*
22: qb_est22:*
23: qb_est23:*
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26: qb_est26:*
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41: qb_est41:*
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43: qb_est43:*

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257: qb_cst177:*
258: qb_cst178:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	711.6	44.0	3607	192	AK004753	AK004753 Mus muscu
2	534.4	33.0	536	143	BF042060	BF042060 Bp250023A
3	519.4	32.1	544	32	AV666882	AV666882 AV666882
4	517	32.0	520	143	BF046412	BF046412 Bp250011A
5	491.4	30.4	493	116	AM465562	AM465562 Bp230019B
6	477.4	29.3	479	116	AM463741	AM463741 Bp230015B
7	473.4	29.3	475	116	AM464433	AM464433 Bp230015B
8	465.8	28.8	523	31	AV603266	AV603266 AV603266
9	416	25.7	549	31	AV603267	AV603267 AV603267
10	390.6	24.2	1370	192	AK015047	AK015047 Mus muscu
11	371.8	23.0	399	32	AV666881	AV666881 AV666881
12	360.4	22.3	362	143	BF042944	BF042944 Bp250002A
13	341.6	21.1	1094	174	BF047143	BF047143 Bp2334132
14	330.4	20.4	333	143	BF040713	BF040713 Bp250002A
15	308	19.0	1207	192	AK016765	AK016765 Mus muscu
16	306.8	19.0	530	143	BF038182	BF038182 Bp250008H
17	297.8	18.4	1229	192	AK016248	AK016248 Mus muscu
18	202.6	12.5	1037	221	CNS040JM	AL268987 Tetradon
19	187	11.6	440	3	AA175441	AA175441 ms87604.r
20	146.4	9.1	416	187	R24770	R24770 y942c11.r1
21	143.8	8.9	670	151	BF612960	BF612960 dg79d10.x
22	137.6	8.5	483	150	BF544312	BF544312 U1-R-BT0-
23	136.2	8.4	743	251	AZ899051	AZ899051 RPI-24-2
24	134.8	8.3	600	237	AZ015258	AZ015258 RPI-23-2
25	131.6	8.1	628	236	AO996632	AO996632 RPI-23-3
26	128.2	7.9	522	148	BF392700	BF392700 U1-R-CA0-
27	125.2	7.7	544	140	BF080178	BF080178 213324 MA
28	125.2	7.7	552	31	AV613965	AV613965 AV613965
29	114.4	7.1	490	146	BF284956	BF284956 B122901.w
30	112.4	7.0	486	118	AM634604	AM634604 U1-R-CA0-
31	109	6.7	481	148	BF394852	BF394852 U1-R-CA0-
32	107.8	6.7	562	165	BF234506	BF234506 141635 MA
33	97	6.0	891	172	BF025899	BF025899 602292041
34	85.2	5.3	943	105	AL525920	AL525920 AL525920
35	82.8	5.1	310	150	BF544313	BF544313 U1-R-BT0-
36	80.2	5.0	568	2	AA088048	AA088048 m001607.r
37	79.4	4.9	518	111	AM118601	AM118601 x934d08.x
38	77.6	4.8	925	219	CNS0091P	AL053013 Drosophila
39	77.2	4.8	935	219	CNS0060X	AL066742 Drosophila
40	76.4	4.7	932	219	CNS0072Q	AL066742 Drosophila
41	76	4.7	473	15	AI025815	AI025815 ov94e10.s
42	72.6	4.5	495	122	AM921899	AM921899 EST353203
43	71.4	4.4	935	219	CNS0060X	AL066742 Drosophila
44	70.4	4.4	318	145	BF193675	BF193675 245344 MA
45	70.4	4.4	321	145	BF193676	BF193676 245345 MA

ALIGNMENTS

RESULT 1
AK004753
LOCUS
DEFINITION
AK004753 3607 bp mRNA HTC 08-FEB-2001
Library, clone:1200014C04, full insert sequence.

ACCESSION
AK004753
VERSION
AK004753.1
KEYWORDS
CAP trapper.
SOURCE
Mus musculus (strain:C57Hl/6J) adult male lung cDNA to mRNA,
clone:1200014C04, full-length enriched mouse cDNA library
clone:1200014C04.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (sites)
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High efficiency full-length cDNA cloning

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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TITLE

JOURNAL

/lab_host="DH10B"

/note="Organ: placenta; Vector: pRTTpac; Site 1: EcorI;

Site 2: NotI. The cDNA library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Ronaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 160 a 111 c 141 g 124 t

ORIGIN

Query Match 33.0%; Score 534.4; DB 143; Length 536;

Best Local Similarity 99.8%; Pred. No. 2.5e-126;

Matches 535; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 545 aaagcccaaaagctcttctgtgataaccatcaagaaccagaagttgttgca 604
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ACAGCCCAAGAGCGCTCTTGTGTGATTAACCCATCAAGAAACCCAGAGTTGGTGGCA 60
 QY 605 gcaagcattcaaaagctctgtgctccagatggttlaacaatggttlaacaagaag 664
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GCAGCATTCAGAGAGGCGCTGTGCTTCCAGATGCTTTAACATATGTTACCATGAGAGAG 120
 QY 665 atggaacataaagcaagaagaacaaagaacgaagaacgaagaacgaagcttaagctat 724
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ATGAGACATTAACGAGAAAGCAAAAGCAAGCAAGCAAGCAAGCTTAACCTAT 180
 QY 725 cggactggttcaacccatttaaacgccccgaggtgtgacatgacgaagtgaagcttc 784
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CGGACTGGTTCAACCCATTTAAACGCCCGAGGTTGTGACATGAGAGAGTGAAGAGCTTC 240
 QY 785 caatggtgtggaaggaagcattacaacagagccgtcttaacaattatagccaacaga 844
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CACTGGTGTGGAGAGGACTTACAACAGAGCCCTTTAGCAATTTATGCGCAACAGCA 300
 QY 845 aaattacccgtcgactgacggttttcgcccgtcggagaatatacttgaacttgaag 904
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AAATTACCTCGGCTGACGGTTTTCGCGTGGAGATATGATGAGCATTTACTTGGAG 360
 QY 905 agttcttaacgtctgtcttaataagcattatgtgtggtccacagtcattcttataata 964
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 AGTTCTTAAGCTGTCTTAATAAGACCTTCATGTTGGCCACCCAGCATCTTTATATGA 420
 QY 965 tggatagatggtctcccaagatgccttataagtttggctcctcgccctctttaaag 1024
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 TGTATATATGATCTCTCCAGATGCTCTTTGATAGATTTGGTCTCTCGCTCTCTTAAG 480
 QY 1025 tggtaagatcaagccttgagaagaagtggaagacatcagatgagcagatgaag 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 TGTTAAGATCAAGCCTGAGAAAGAGGTGGCAGACATCAGCATGATGCGCATGAAG 536

RESULT 3
 AV666882 544 bp mRNA EST 25-AUG-2000
 LOCUS AV666882 Bos taurus adipocyte cell line Bos taurus cDNA clone
 DEFINITION E1AD021G06 5', mRNA sequence.
 ACCESSION AV666882
 VERSION AV666882.1 GI:9925912
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

REFERENCE
 1 (bases 1 to 544)
 Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and

AUTHORS
 Suzuki, H.
 TITLE
 bovine cDNA sequencing
 JOURNAL
 Unpublished (2000)
 CONTACT
 Contact: Yoshikazu Sugimoto
 COMMENT
 Animal Genetics Division
 Shitakawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-shitakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641
 Fax: 81-248-25-5725
 Email: kazu@genetec.co.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

Location/Qualifiers

1..544

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="E1AD021G06"

/clone_id="Bos taurus adipocyte cell line"

/cell_type="an adipocyte cell line"

/lab_host="DH10B"

/note="Vector: pZ11; Site 1: SalI; Site 2: NotI; Poly A

BASE COUNT 165 a 110 c 138 g 131 t

ORIGIN

Query Match 32.1%; Score 519.4; DB 32; Length 544;

Best Local Similarity 99.6%; Pred. No. 1.8e-122;

Matches 531; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 450 aagcagatagagaaacatgaatgctcaagaagaagatgcttcaatgctggtlgt 509
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 12 ACAGCATGAGGAGAAATATATGATGTCAGAGAGAAATGATTCGTGATGCTGTTGT 71
 QY 510 ctcaactgcatgt 569
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 72 CTCACCTGATGTTGTTGTTTGGGAAATATTCACAGCCGAGAGGCTCTTGTGTTG 131
 QY 570 gataaacccatcaaaaaccagaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 629
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 132 GATTAACCCATTAAGAAACCCAGAGTTGTTGTCAGACATTCAGAAAGGCTGTTGCT 191
 QY 630 tccgagatggttcaaatggttaccatgaagaagaatgagacataaagcaagaagaaga 689
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 192 TCCGAGATGTTTAAACATATGCTTACCATGAAACATGAGATGAGATTAAGAAAGAA 251
 QY 690 acaagaagaac-cgaagaagcaagaagcctaagctatcgagatggttcaacccattaaac 748
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 252 ACAAGAAACCCAGAAACCCAGAAACCCAGCTTAACCTATCCGACGTTCAACCATTTAAC 311
 QY 749 gccccgaggtgtgacatgaagaagtggaagctccagtggtgtgtgtgtgtgtgtgt 808
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 312 GCCCGAGGTTGTGACATGACGAGAGTGAAGGCTCAGTGTGTGGAAGGCACTTACA 371
 QY 809 acaagacgcttcaacaattatagccaagcagaataatccgtcgccgtgaagctt 868
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 372 ACAGAGCGCTTTAGCAATTTATGCGCAACAGCAAAATTAACGCTCGCGCTGACGTTT 431
 QY 869 tgcgctcggaagatacattgagcatttgaagagagtttcttaacgtctgctaaagc 928
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 432 TCGCGCTCGAGAGATATGATGAGCATTTACTTGGAGAGTTCTTAACGCTGTCTATAAGC 491
 QY 929 acttcatggt 981
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 492 ACTTCATGTTGTGCGCACCCAGCATCTTTATATATGATGATGATGATGCTGC 544

RESULT 4
 BF046412 520 bp mRNA EST 10-OCT-2000
 LOCUS BF046412 BP250011A20E3 Soares normalized bovine placenta Bos taurus cDNA
 DEFINITION clone BP250011A20E3 5', mRNA sequence.
 ACCESSION BF046412
 VERSION BF046412.1 GI:10763467
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

REFERENCE
 1 (bases 1 to 520)
 Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and

AUTHORS
 Suzuki, H.
 TITLE
 bovine cDNA sequencing
 JOURNAL
 Unpublished (2000)
 CONTACT
 Contact: Yoshikazu Sugimoto
 COMMENT
 Animal Genetics Division
 Shitakawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-shitakawa, Fukushima 961-8061, Japan

D	b	1	GGCCCGAGCATTGTACCATGACCAAGTGGAAAGGCTCCAGCTGCTGTGGGAAGGCATTTACA	60
O	y	809	acgaagccgctccttagacaattatattatgcagaagcaadaaltaaccctgacctgaaggctt	868
D	b	61	ACAAAGCCCTCTTGACAAATATATATATGCCAAGCAGAAAATAATTCGCGCTGCAGCGTTT	120
O	y	869	tccggcttcgaaagtataattagacttaactctggaggagttctctaactcttactataagc	928
D	b	121	TGGCGCTGCAGAACATACACTTAGGCAATTACTTGGAGAGATTCTTAACGCTCTCTAATAAGC	180
O	y	929	acttcatggttgagcgcaaccacatcatcttatcatatgatgatgatcttccaagatgc	988
D	b	181	ACTTCATGCTTGCGCCAGCGCACATCATCTTTATATCAATGCTAGATGATGTCTCCAGAGATGC	240
O	y	989	ccttcatagaaatttaggttcctctcagcctccttcaaagttttaagatcaagccctgagaaga	1048
D	b	241	CTTGCATAGAGTTTGAGTTCCTCTGCGCTCTCTCAAAGTTTATAGATCAAGCCTGAGAGA	300
O	y	1049	ggttcgcagagatatagatagtatgcccataagaaactatctggaggagaaacttgtgccacca	1108
D	b	301	GCTGCGACGACATPACGATATGATGGCATGGAAGACTATCGGAGACATCTGTGCGCCACA	360
O	y	1109	tccagcatgaagcttgaactccttcttcatcatgatatgtagcaagctcttccaagaagaat	1168
D	b	361	TCCAGCATGAGCTTGACTTCCTTTCTTCATGATGATGTGGACCAGSTCTTCCAGAGCAAGT	420
O	y	1169	ttcaagatagagaagcccttgagcgaatcagtgccccagcctaacaaqctctgtgtacaaagcag	1228
D	b	421	TTGGGCTGGAGAACCTTGCGCGAGTGGCGGCCAGCTCAAGGCGTGGTACAAAGGCAG	480
O	y	1229	atcccaaatgaactt 1241	
D	b	481	ATGCCAATGACTT 493	
RESULT 6				
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LOCUS				
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DEFINITION BP230013B10G8 Soares normalized bovine placenta Bos taurus cDNA				
clone BP230013B10G8 5', mRNA sequence.				
ACCESSION AM463741				
VERSION AM463741.1 GI:7033909				
KEYWORDS EST.				
SOURCE com.				
ORGANISM Bos taurus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
Bovidae; Bovinae; Bos.				
REFERENCE 1 (bases 1 to 479)				
AUTHORS Lewin,H.A., Soares,M.B., Rebeitz,M., Pardinas,J., Liu,L. and Larson,				
J.H.				
TITLE Bovine ESTS				
JOURNAL Unpublished (2000)				
COMMENT Contact: Lewin, H. A.				
W. M. Keck Center for Comparative and Functional Genomics				
University of Illinois at Urbana-Champaign				
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL				
61801, USA				
Tel.: 217 343 5998				
Fax: 217 244 5617				
Email: h-lewin@uiuc.edu				
Funding for cattle EST sequencing was provided by the USDA National				
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534				
to H. A. Lewin and J. F. Womack. Base Calling/Quality Scores: PHRED				
from Washington University Genome Center. Vector Trimmi g:				
Cross-match from Washington University Genome Center PHRAP suite.				
Sequences submitted are vector free and at least 200 bp in length.				
PCR primers				
FORWARD: TAATATGATCTACTATAGCG				
BACKWARD: ATTAAAGCTCCTACTAAG				
Insert Length: 479 Std Error: 0.00				
Plate: BP230013B10 row: G column: B				
Seq primer: AGCGGATACAAATTTGCACACGCA				

FEATURES					
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	/clone="_BP230013BI0C8"				
	/_clone_lib="Soares normalized bovine placenta"				
	/sex="female"				
	/lab_host="DH10B"				
	/note="Organ: Placenta; Vector: pT7SPac; Site-1: EcoRI;				
	Site-2: NotI; The cDNA library was contributed by the				
	Soares laboratory and it was constructed and normalized				
	as described by Bonaldo, M.F., Lennon, G. and Soares,				
	M.B. (1996), Genome Research 6(9): 791-806."				
BASE COUNT	142 a	102 c	122 g	113 t	
ORIGIN					
Query Match	29.5%;	Score 477.4;	DB:116;	Length 479;	
Best Local Similarity	99.8%;	Pred. No. Jc=111;			
Matches 478;	Conservative	0:	Mismatches 1;	Indels 0;	Gaps 0
OY	545	acaagccagaagqgccttattatcttgataaacccaaccaaaaccagaagttaagtga	604		
Db	1	ACACCAGAAGGCTCTTTTGTCTGGATTAACCCATCAGAAACCAAGTAGTGSTGSCA	60		
OY	605	qcaacattcagaaggctgtggttcgccagatgatttaacaaigtllaccatgaagaag	664		
Db	61	GCACATTTCAGAAAGGCGTGGCTGCCATCCAGATGGTTTACCATGTTACCATGAAG	120		
OY	665	atggagacataaaggaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag	724		
Db	121	ATGAGACATTAACGAAGAAAGAACAAAGAAAGAAAGAAAGAAAGAAAGCTTAAGCTAT	180		
OY	725	cgaacttgatlcaaccattlaaagcccgaagtttgtaccatacgaaagtggaaagctc	784		
Db	181	CGGACTGGTTCAACCCATTTAAGCGCCCGCAGTGTGTGACATGACGAAGTGGAAAGGCTC	240		
OY	785	caatgttgtggaagcaacttacaaagacgcltttagacaattatatgcacaagaca	844		
Db	241	CAGTGGTGTGGGAAGGCACCTTACACAAGACCCTCTTACACATTATTATGGCAAGACA	300		
OY	845	aaattaccgttcgcttgacggcttttcgcgttggaaagataaatgaattacttggag	904		
Db	301	AAATTACCGTCGCGCTACGCGTTTTGCGCGTCGGAAGATPACATTGACATTACTTGAGG	360		
OY	905	agctcttaacgtctgcctaataagaaccttcatgttgagccaccagctatctttatcaa	964		
Db	361	AGCTCTTAACGCTGCTGCTAATAAGCACCTTCATGTTGGCCACCCAGTCACTTTATATCA	420		
OY	965	tgttatagatgatgtccagaagatgcctttgatagaagtgtgctctctgcctctcaaa	1023		
Db	421	TGTTAGATGATGTCCTCCAGATGCTCTTGTATAGATTGGGTCTCTCTGCGCTCTTCAAA	479		
RESULT	7				
AM464433					
LOCUS	475 bp	mRNA	EST	24-FEB-2000	
DEFINITION	BP230015B20C5 Soares normalized bovine placenta Bos taurus cDNA				
ACCESSION	AM464433				
VERSION	AM464433.1	GI:7034601			
KEYWORDS	EST.				
SOURCE					
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 475)				
AUTHORS	Lewin,H.A., Soares,M.B., Rebelz,M., Pardinas,J., Liu,L. and Larson				
	J.H.				
TITLE	Bovine ESTs				
JOURNAL	Unpublished (2000)				

COMMENT

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Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewis and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trim: g: Cross match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
PCR primers

FORWARD: TAATACCTGCTACTATAGG
REVERSE: ATTATCTGCTACTAAG
Insert Length: 475 Std Error: 0.00
Plate: BP240015R20 Row: C Column: 5
Seq primer: ACCGATACCAATTCACACAGA
High quality sequence stop: 475.

FEATURES

SOURCE

Location/Qualifiers
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/organism "Bos taurus"
/db_xref "taxon:9913"
/clone "BP240015R20C5"
/clone_1id "Scars normalized bovine placenta"
/sex "female"
/lab_host "M1010B"
/note "Organ: placenta; Vector: p778Frac; Site_1: EcoRI; Site_2: NotI; The cDNA library was constructed by the Scars Laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lomon, G., and Soares, M.B. (1996). Genome Research 6(9): 791-806."

BASE COUNT
159 a 101 c 122 g 113 t
ORIGIN

Query Match 29.4% Score 47.4; DB 116; Length 475;
Best Local Similarity 99.8% Pred. No. 1 to 110;
Matches 474; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

545 atgagccagagagctcttctgataaacacacagagagagagagatgagga
1 atgagccagagagctcttctgataaacacacagagagagagagatgagga
605 ggcagagctcagagagagctcttctgataaacacacagagagagagatgagga
61 ggcagagctcagagagagctcttctgataaacacacagagagagagatgagga
665 atgagagctcagagagagagagagagagagagagagagagagagatgagga
121 atgagagctcagagagagagagagagagagagagagagagagagatgagga
725 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
181 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
785 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
241 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
845 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
901 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
905 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
961 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
965 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1021 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1025 ggcagagctcagagagagagagagagagagagagagagagagagatgagga

RESULT 8

AV604266 523 bp mRNA EST 40-AUG-2000
AV604266 Bos taurus kidney testis Bos taurus cDNA clone E1K1015811
3', mRNA sequence.

AV604266 1 G1:9725592
EST.
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 523)
Suzuki, Y., Hirotsune, S., Takasuga, A., Tob, R., Uehara, A. and
Suzuki, H.

bovine cDNA sequencing
Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Otsukura, Nishio, Nishi-Shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cc.otsu.ac.jp
Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1..523
/organism "Bos taurus"
/db_xref "taxon:9913"
/clone "E1K1015811"
/clone_1id "Bos taurus kidney testis"
/tissue_type "kidney"
/dev_stage "fetus"
/lab_host "M1010B"
/note "Vector: p211; Site_1: SalI; Site_2: NotI; Poly A was deleted from a NotI site"

BASE COUNT
152 a 111 c 116 g 164 t
ORIGIN

Query Match 28.8% Score 465.8; DB 11; Length 523;
Best Local Similarity 99.6% Pred. No. 1 to 108;
Matches 467; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1149 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
523 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1209 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
463 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1269 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
403 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1329 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
343 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1389 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
283 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1449 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
223 ggcagagctcagagagagagagagagagagagagagagagagagatgagga
1509 ggcagagctcagagagagagagagagagagagagagagagagagatgagga


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|||||
Db 163 GGAATTAACCTGTGACAGATGCTTGGCAGACAAAGATATATGCTGTAATTA 104
QY 1569 tgcctacttctgctgacatcttctgaatttgaagagatattct 1617
Db 103 TGTCTACTTGTGGCAGATGCTGTAATTTGAGAGAGATATTATCT 55

RESULT 9
AV603267 549 bp mRNA EST 30-AUG-2000
LOCUS AV603267 Bos taurus kidney fetus Bos taurus cDNA clone EIK1015B11
DEFINITION 5', mRNA sequence.
ACCESSION AV603267
KEYWORDS AV603267.1 GI:9725593
SOURCE EST.
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
            Ruminantia; Bovidae; Bos.
            1 (bases 1 to 549)
            Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
            Suzuki, H.
            bovine cDNA sequencing
            Unpublished (2000)
            Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shikawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@ecora.ocn.ne.jp
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
            Location/Qualifiers
            1..549
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone="EIK1015B11"
            /clone_1ib="Bos taurus kidney fetus"
            /tissue_type="Kidney"
            /dev_stage="Fetus"
            /lab_host="DH10B"
            /note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
            was deleted from a NotI site"

BASH COUNT 154 a 125 c 152 g 118 t

Query Match 25.7%; Score 416; DB 31; Length 549;
Best Local Similarity 97.7%; Pred. No. 66-96;
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 326 caactcacaaatcaacgagatcagaagctgacacttgcctcccccgcctcctc 385
Db 118 CAGCAATATACAGACAGTACAGTACAGAGCTGCACCTTCCTTCCTCCACGCCCTGCTC 177
QY 386 cttctgcaagaagagctcagtaagacttgaacttgccttllactctagaagagag 445
Db 178 CTCTGACAGACGACCTCAGTAGAATCTTGACTTTTACTCTTACTAGSAGAGAG 237
QY 446 aagcagacgagatgaagaaataatgaatgtcgaagaaagagatgctcgaatctg 505
Db 238 AACGACGATGAGGAGAAATATCAATCTCAAGCAAAAGTATTCCTCAATCTG 297
QY 506 ttctctcaacttgcattgttcttllggaatatatccacagcccaagagctcttga 565
Db 298 TTGCTCAACTGTCATTTGTTGTTGGCAATATATCCACAGCCAGAGAGGCTCTTTGT 357
QY 566 tctgataaaccatcaagaaccagaaatgtgtgagcaagacattcagaagagctgct 625
Db 358 TCTGATAAACCATCAAGAAACCAAGAACTGCTGTCACAGCATTGACAGAGGGTGGT 417

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QY 626 agcttccagatggtlltaacaatggtllaccatgaagaagatgagacataacgaagaa 685
Db 418 GCGTTCGAGATGCTTTAAACAATGCTTACCATGAAAGAAATGACACATAAACGAAGAAA 477
QY 686 aggaacaaagaacgaagacgaagaaacttaagctatcgaactgtcttccatctta 745
Db 478 AGGAAACAAAGAAACGACAGCAACGCAAGCTTAAGCTATGAGCTAGTTCAGACCATTTA 537
QY 746 aagcgcgcagag 757
Db 538 AACGCCCGCAGG 549

RESULT 10
AK015047 1370 bp mRNA HTC 08-FEB-2001
LOCUS AK015047 Mus musculus adult male testis cDNA, RIKEN full-length enriched
DEFINITION library, clone:4930402F06, full insert sequence.
ACCESSION AK015047
VERSION AK015047.1 GI:12853236
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain:c57BL/6J) adult male testis cDNA to mRNA,
            clone:4930402F06.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (sites)
            Carninci, P. and Hayashizaki, Y.
            High-efficiency full-length cDNA cloning
            Methods Enzymol. 303, 19-44 (1999)
            2 (sites)
            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
            Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
            Genome Res. 10 (10), 1617-1630 (2000)
            3 (sites)
            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
            Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
            Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T.,
            Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T.,
            Kasai, W., Fujiwara, S., Inoue, K., Tozawa, Y., Izawa, K., Ohara, E.,
            Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
            Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
            Genome Res. 10 (11), 1757-1771 (2000)
            4 (sites)
            FANTOM Consortium.
            FANTOM Genome Exploration Research Group Phase 11 Team and
            FANTOM Consortium.
            Functional annotation of a full-length mouse cDNA collection
            Nature 409, 685-690 (2001)
            5 (bases 1 to 1370)
            Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
            Arikawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
            Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F.,
            Imocani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
            Kojima, Y., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T.,
            Miyazaki, A., Nishi, K., Momura, K., Numaizaki, R., Ohno, M., Okazaki, Y.,
            Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,
            Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T.,
            Soabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
            Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
            Tanaka, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
            Direct Submission
            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

```


FEATURES	source
ORGANISM	COW.
REFERENCE	Hos taurus
REFERENCE	Enkaiyotia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
REFERENCE	Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 362)
REFERENCE	Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
REFERENCE	J. H.
REFERENCE	Bovine ESTs
REFERENCE	Unpublished (2000)
REFERENCE	Contact: Lewin, H. A.
REFERENCE	W. M. Keck Center for Comparative and Functional Genomics
REFERENCE	University of Illinois at Urbana-Champaign
REFERENCE	340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
REFERENCE	61801, USA
REFERENCE	Tel: 217 333 5998
REFERENCE	Fax: 217 244 5617
REFERENCE	Email: h-lewin@uiuc.edu
REFERENCE	Funding for cattle EST sequencing was provided by the USDA National
REFERENCE	Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
REFERENCE	to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
REFERENCE	from Washington University Genome Center. Vector Trimmi g:
REFERENCE	Cross-match from Washington University Genome Center PHRAP suite.
REFERENCE	This sequence is vector free and at least 200 bp in length.
REFERENCE	PCR primers
REFERENCE	FORWARD: TAAATGCACTGACTATAGCG
REFERENCE	BACKWARD: ATTAAGCCCTGACTAAAG
REFERENCE	Insert Length: 362 Std Error: 0.00
REFERENCE	Plate: Bp250002A10 row: F column: 3
REFERENCE	Seq primer: AGCGATATACAAATTTCACACGGA
REFERENCE	High quality sequence stop: 362.
REFERENCE	location/Qualifiers
REFERENCE	1..362
REFERENCE	/organism="Bos taurus"
REFERENCE	/db_xref="taxon:9913"
REFERENCE	/clone="Bp250002A10F3"

	BASE COUNT	103 a	78 c	90 g	91 t	
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Query Match	22.3%	Score 360.4:	DB 143:	Length 362:		
Best Local Similarity	99.7%	Pred. No. 1e-81:				
Matches 361:	Conservative	0:	Mismatches	1:	Indels	0:
Gaps						0:
OY	681	aagaaaggacaaaagaacgaacgaaacgaacgttaacgtatcgaatqattvaacc	740			
Dd	1	AGAAAAGGACAAAGAACGAAGACGAAAGCAAGCTTAAGCATCGAATGGTTCACGCC	60			
OY	741	attaacgcgcccgaggtgttgaccatgaacgaacgaacgaacgtctcaagtatgaagaag	800			
Dd	61	ATTAAAGCCGCCCGCAGGTCTTGACCATGCACGAAGTGGAGGCTCCAGTGGTTGGGAAGG	120			
OY	801	cacttacaacgaacgcgtctttgaacaaallatalatcccaaggaacaaataacgcctgcct	860			
Dd	121	CAGTTACAAACACCGCGCTCTTAGACAATAATTATATGCAAGCACAAAAATATCCGTGGGCT	180			
OY	861	gacggttttcgcgtcgaagatatcattdagcatlacttgaagaatctctaagctctac	920			
Dd	161	GACGGTTTTGCGCGTCGCAAGATACATTGAGCATTTACTTGGAGGANTTTTAAAGCTGCG	240			
OY	921	tataaacgaacttcalqtatggacacccaagtcacttttatattatgaatgaatgatctc	980			
Dd	241	TAAATAGCACTTCATGHTGGTGGCCACCACTCATCTTTATATCAATGGTATGATATGTC	300			
OY	981	caagatgacctttgaataaatltgaatctctctgcgcctcttcaaagctlllaadattaaacc	1040			
Dd	301	CAGGATGCCCTTGATAGACTTGSGHCTCTGCGCTCTCCAAGTOTTTAACATTAAGGCC	360			
OY	1041	tg 1042				
Dd	361	TG 362				
RESULT 13						
LOCUS	BC174143	1094 bp	mRNA	EST	06-FEB-2001	
DEFINITION	602334121 NCL_CGAP_Mami Mus musculus cDNA clone IMAGE:4457344	5'				
ACCESSION	BC174143					
VERSION	BC174143.1	GI:12680846				
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Scleromorphi; Muridae; Murinae; Mus.					
TITLE	Nih-MGC http://mgc.nhl.nih.gov/.					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
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	Tissue Procurement: Gilbert Smith, Ph.D.					
	cDNA Library Preparation: Life Technologies, Inc.					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNI at:					
	http://image.llnl.gov					
	Plate: L1AM10253 row: P column: 07					
	High quality sequence stop: 662.					
	Location/qualifiers					
FEATURES						

QY 975 tttctccaggatgcctttgataaqaattggatcc 1007
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Db 301 TGTCTCCAGCATGCTTTGATAGAGTTGGCTGC 333

